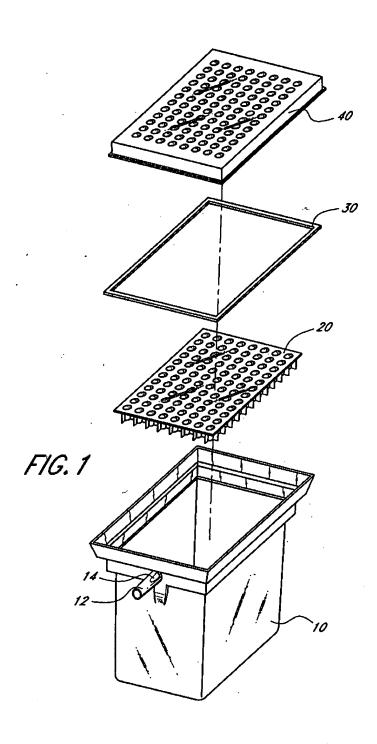
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Figures and Drawings



Device and Method For High-Throughput Quantification of MRNA From Whole Blood

Masato Mitsuhashi

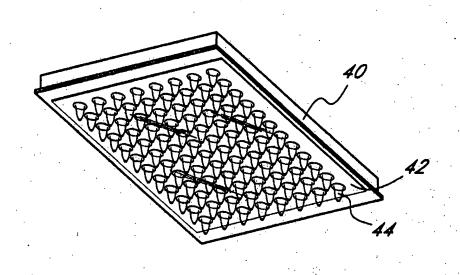


FIG.2

FIG 3. Efficiency of leukocyte trapping of fresh and frozen blood samples on filterplates

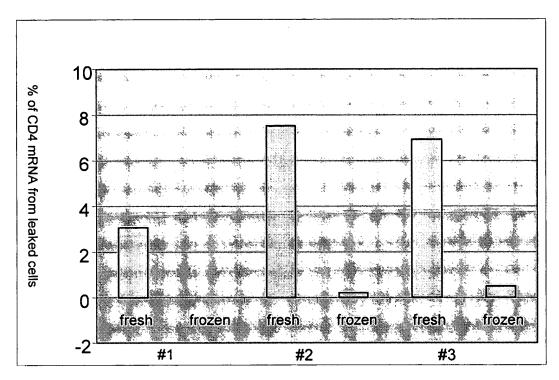


FIG 4. Number of washes after application of blood

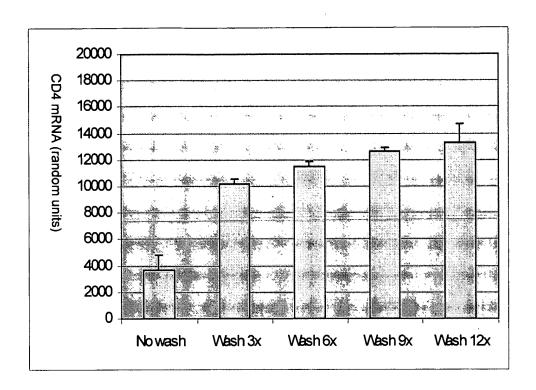


FIG 5. Final treatment of filterplate before cell lysis

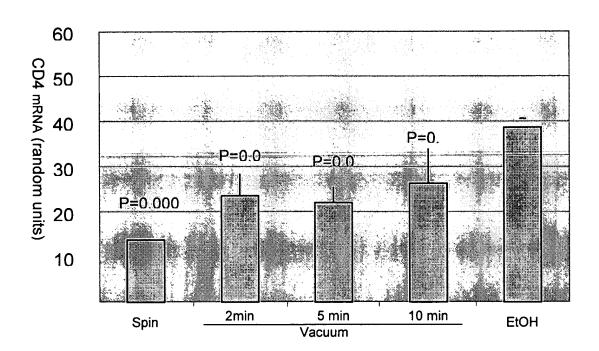
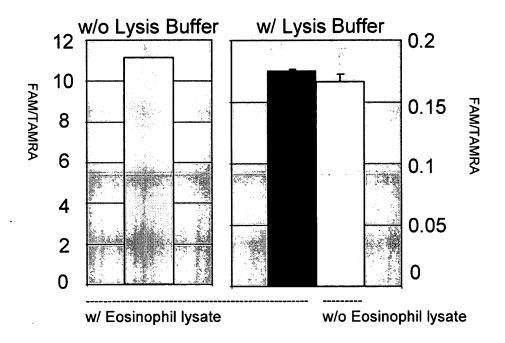


FIG 6. Lysis Buffer: RNase inhibition



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FIG 7. Optimal concentrations of reverse transcriptase

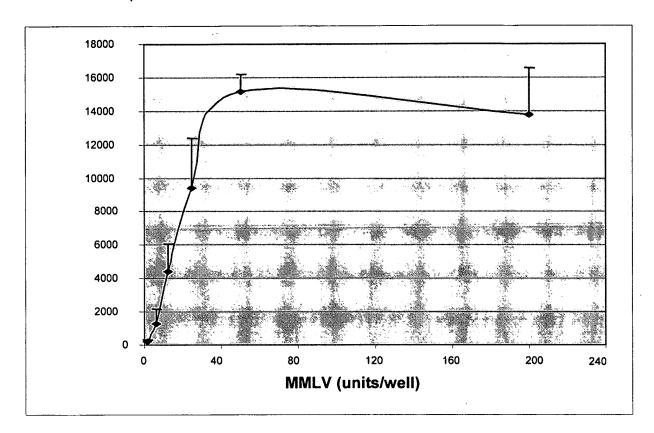


FIG 8. Optimal volume of cDNA for PCR

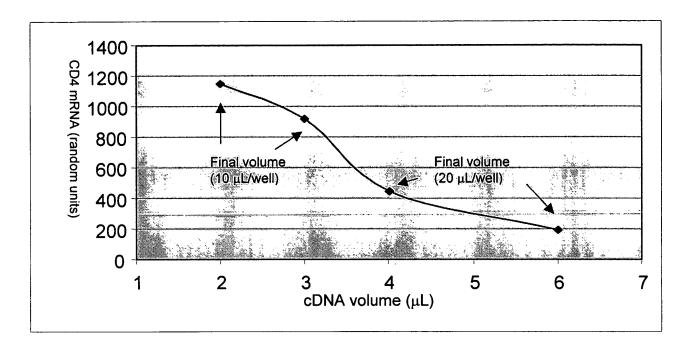


FIG 9. Hybridization kinetics

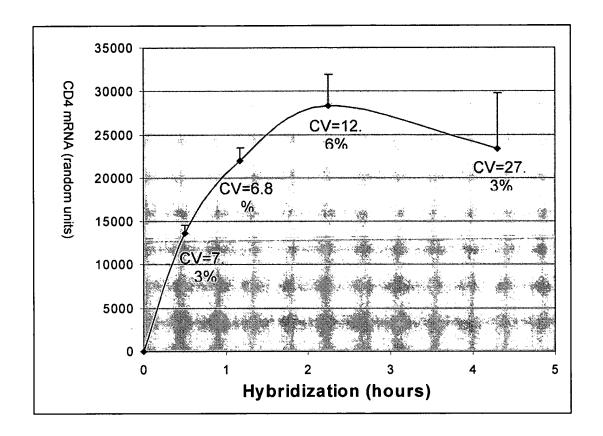


FIG 10. Blood volume

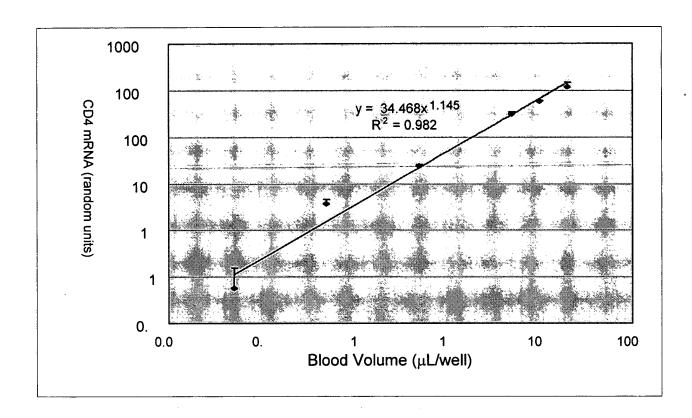
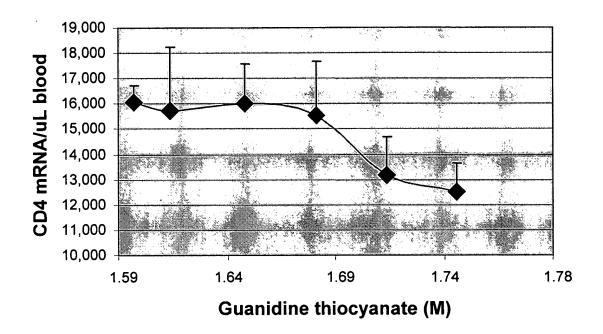
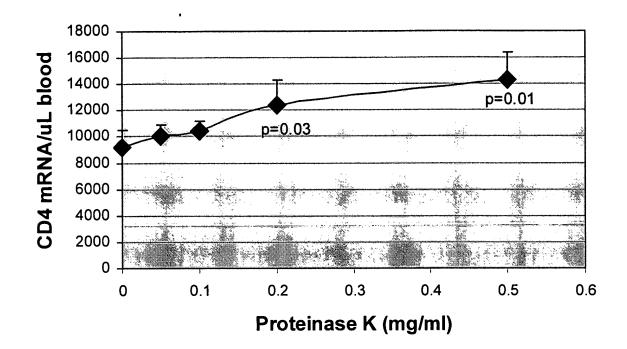


FIG 11. Optimal guanidine thiocyanate concentration.



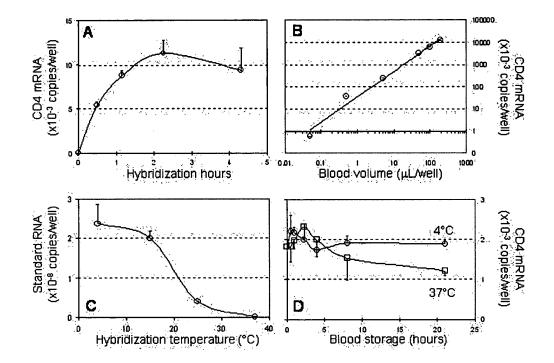
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FIG. 12. Optimal proteinase K concentration.



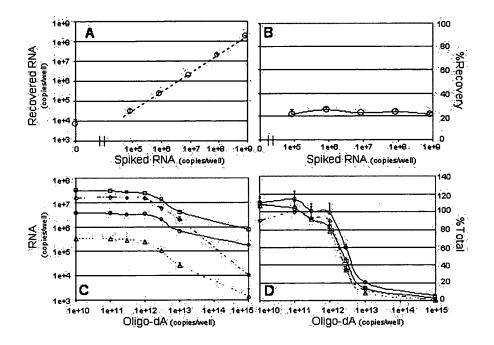
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FIGs. 13A-13D. Assay Validation.



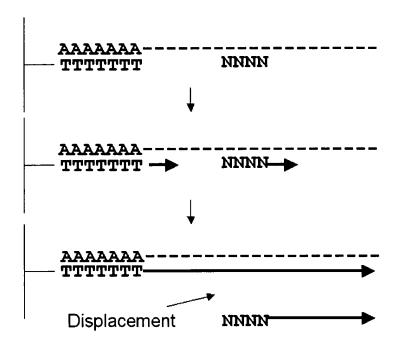
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FIGs. 14A-14D. Recovery of Synthetic Spiked RNA.



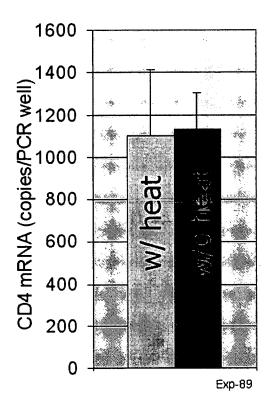
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FIG 15. cDNA synthesis from both specific antisense primer (NNN) and immobilized oligo(dT).



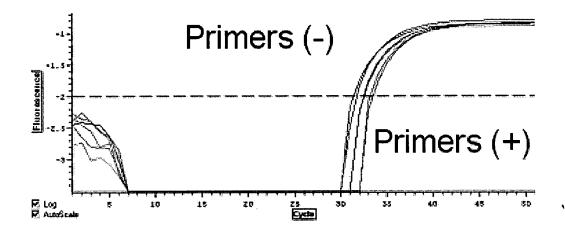
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FIG 16. Recovery of specifically primed RNA with and without denaturization.



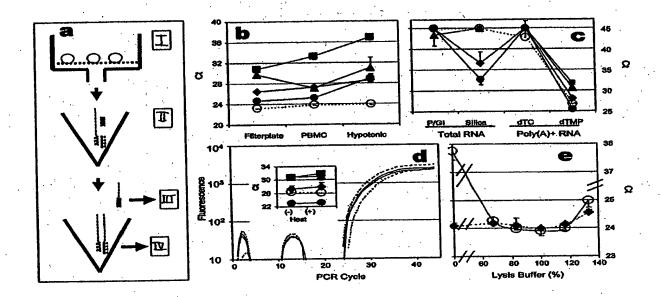
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FIG 17. Amplification of RNA with and without specific primers.

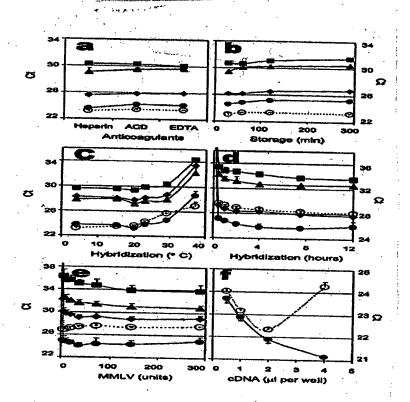


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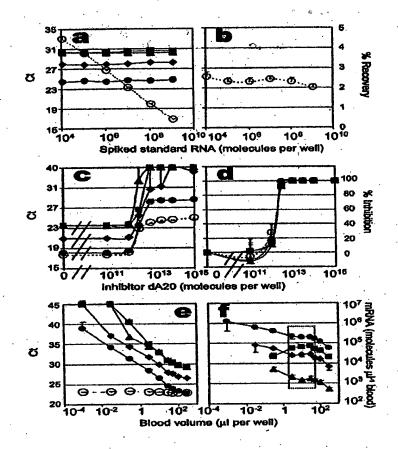
FIGs 18A-18E. mRNA quantification scheme using control RNA.



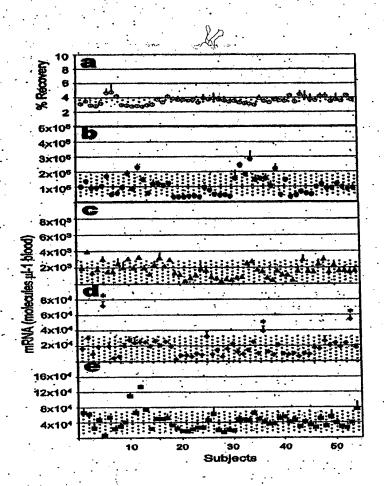
Figures 19A-F. PCR cycles.



Figures 20A-20F. Performance of Control RNA.



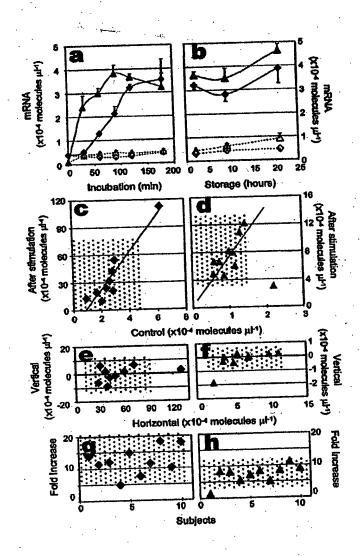
FIGs 21A-E. mRNA recovery of various subjects.



Appl. No.: Not Yet Assigned

Atty Docket: HITACHI.055CP2

Figures 22A-22E. Recovery of mRNA among various subjects.



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